Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:06:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080789.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3080789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:06:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,755,401
Mapped reads	1,583,763 / 90.22%
Unmapped reads	171,638 / 9.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,195 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	57,214 / 3.26%
Duplication rate	3.03%
Clipped reads	817,098 / 46.55%

2.2. ACGT Content

Number/percentage of A's	30,203,321 / 29.13%
Number/percentage of C's	19,601,565 / 18.91%
Number/percentage of T's	32,000,519 / 30.87%
Number/percentage of G's	21,860,962 / 21.09%
Number/percentage of N's	2,097 / 0%
GC Percentage	40%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.2696

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

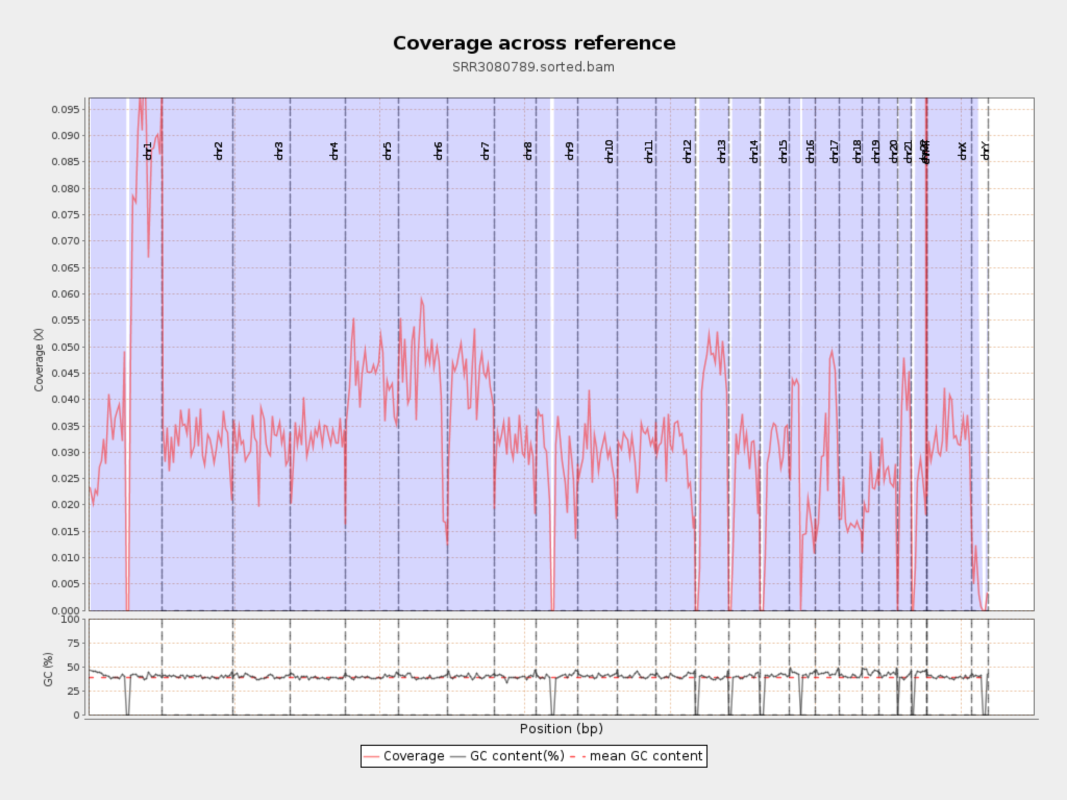
General error rate	0.76%
Mismatches	776,484
Insertions	7,866
Mapped reads with at least one insertion	0.49%
Deletions	22,510
Mapped reads with at least one deletion	1.41%
Homopolymer indels	47.23%

2.6. Chromosome stats

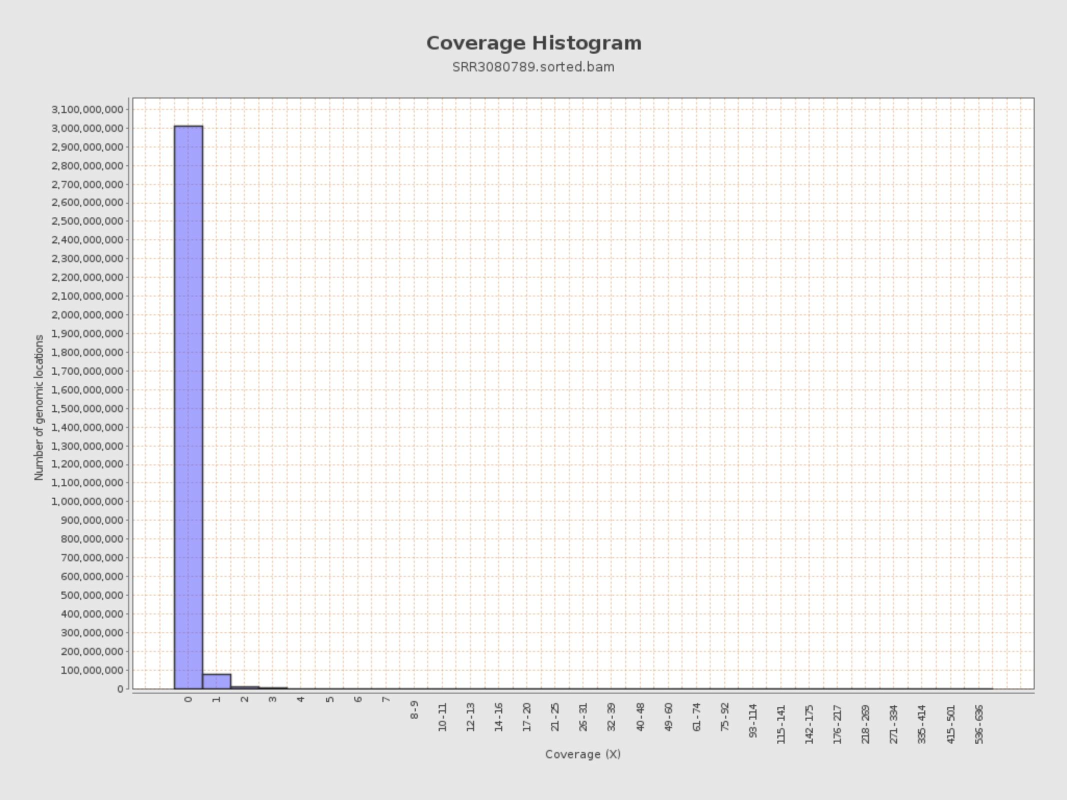
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13335932	0.0535	0.4211
chr2	243199373	7856035	0.0323	0.2845
chr3	198022430	6331607	0.032	0.205
chr4	191154276	6241770	0.0327	0.2133
chr5	180915260	7976426	0.0441	0.2416
chr6	171115067	7630687	0.0446	0.2697
chr7	159138663	7036034	0.0442	0.3403

chr8	146364022	4540252	0.031	0.4236
chr9	141213431	3675595	0.026	0.2206
chr10	135534747	4011666	0.0296	0.2422
chr11	135006516	4199561	0.0311	0.2211
chr12	133851895	4012693	0.03	0.2006
chr13	115169878	4505406	0.0391	0.2284
chr14	107349540	2706191	0.0252	0.1883
chr15	102531392	2631289	0.0257	0.1898
chr16	90354753	2199712	0.0243	0.1863
chr17	81195210	2627742	0.0324	0.2125
chr18	78077248	1337269	0.0171	0.3611
chr19	59128983	1323445	0.0224	0.2938
chr20	63025520	1639443	0.026	0.1865
chr21	48129895	1630897	0.0339	0.2165
chr22	51304566	870514	0.017	0.1471
chrMT	16571	44184	2.6663	2.1613
chrX	155270560	5103846	0.0329	0.2178
chrY	59373566	235849	0.004	0.0955

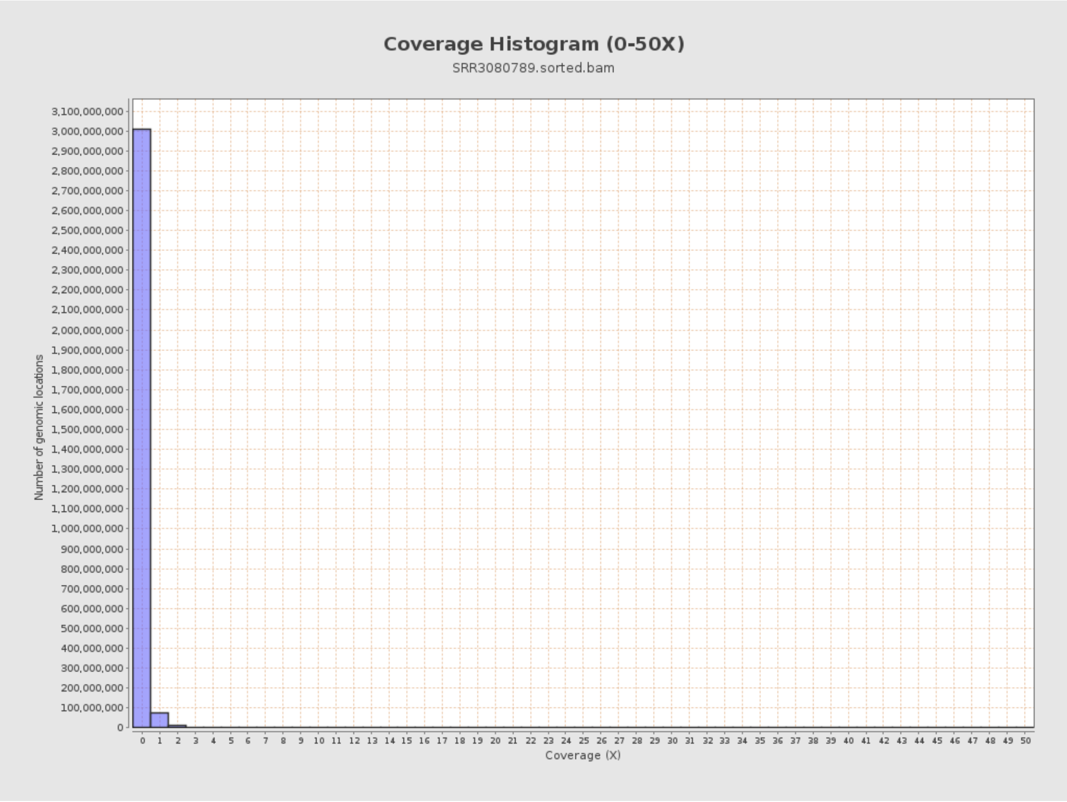
3. Results : Coverage across reference



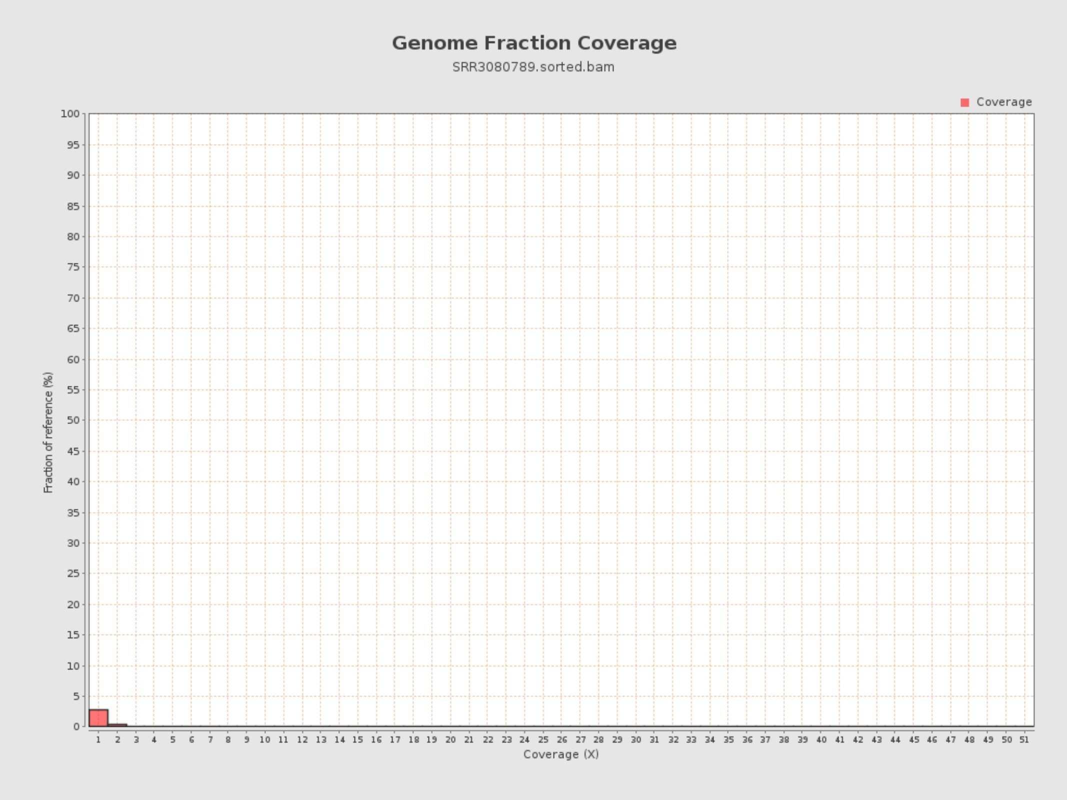
4. Results : Coverage Histogram



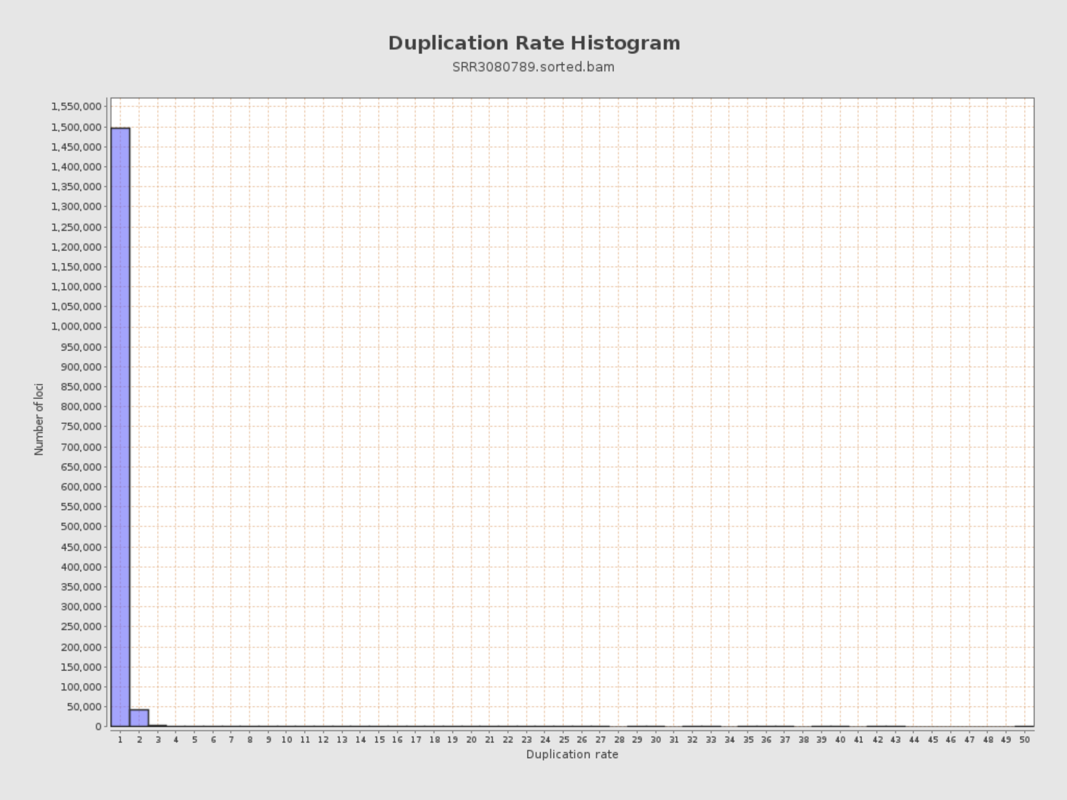
5. Results : Coverage Histogram (0-50X)



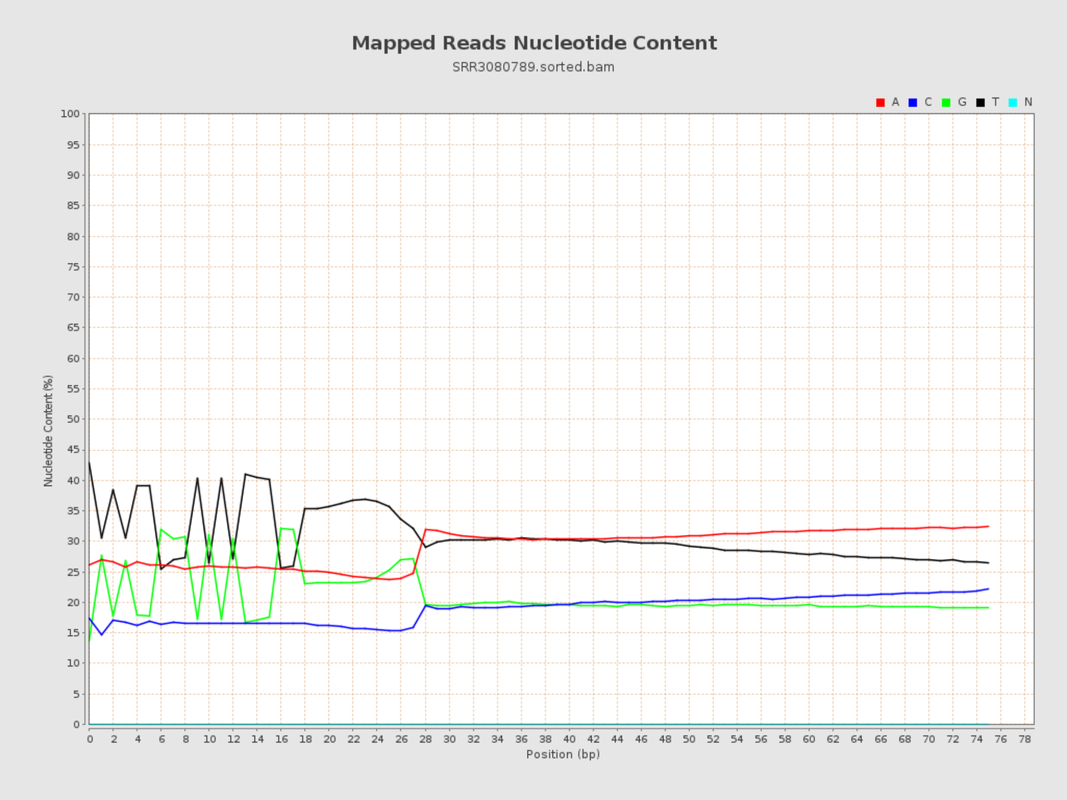
6. Results : Genome Fraction Coverage



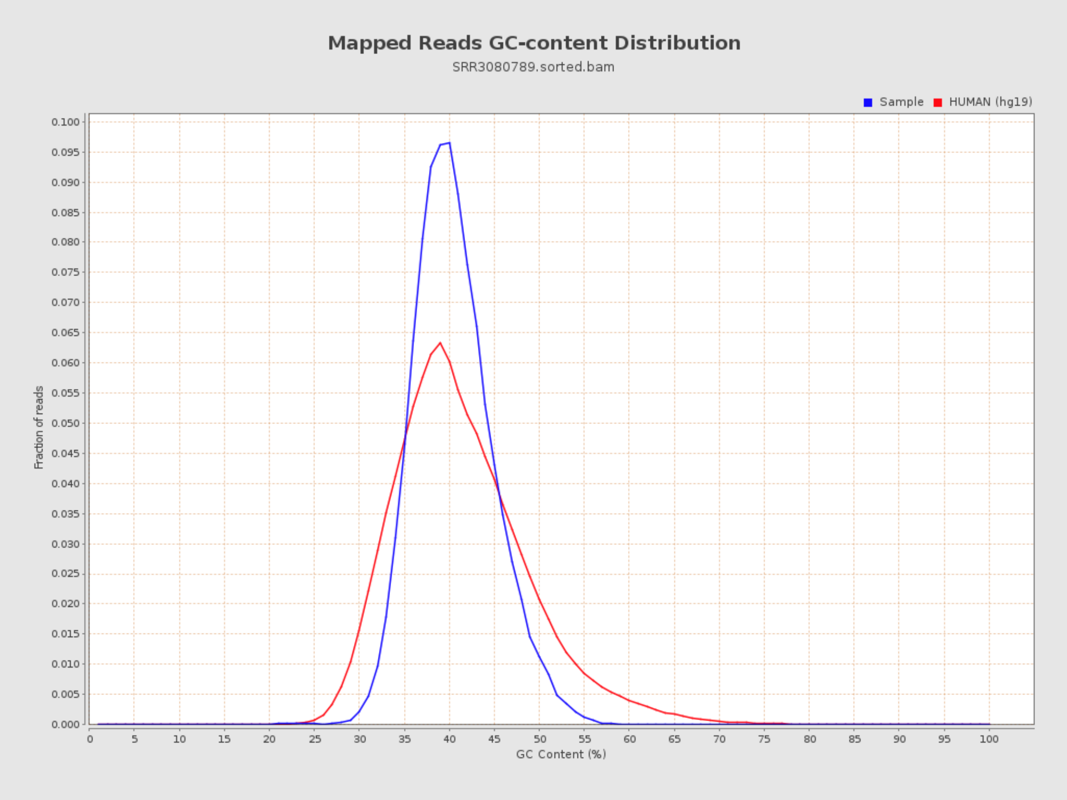
7. Results : Duplication Rate Histogram



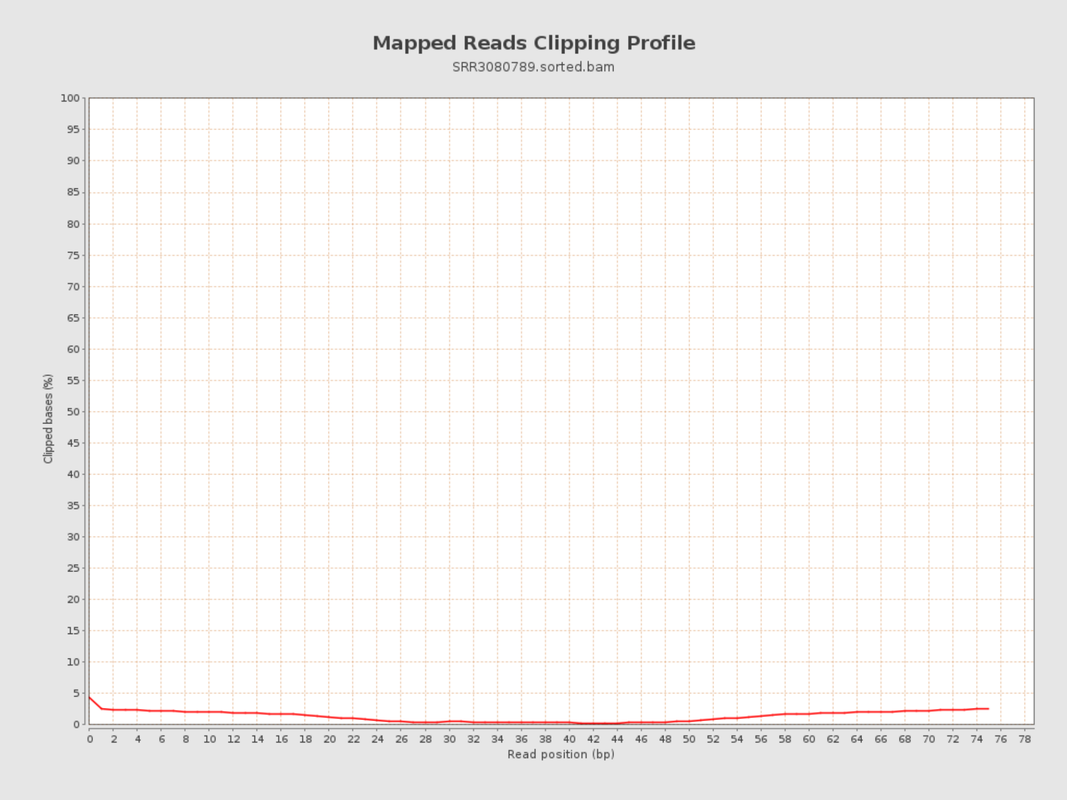
8. Results : Mapped Reads Nucleotide Content



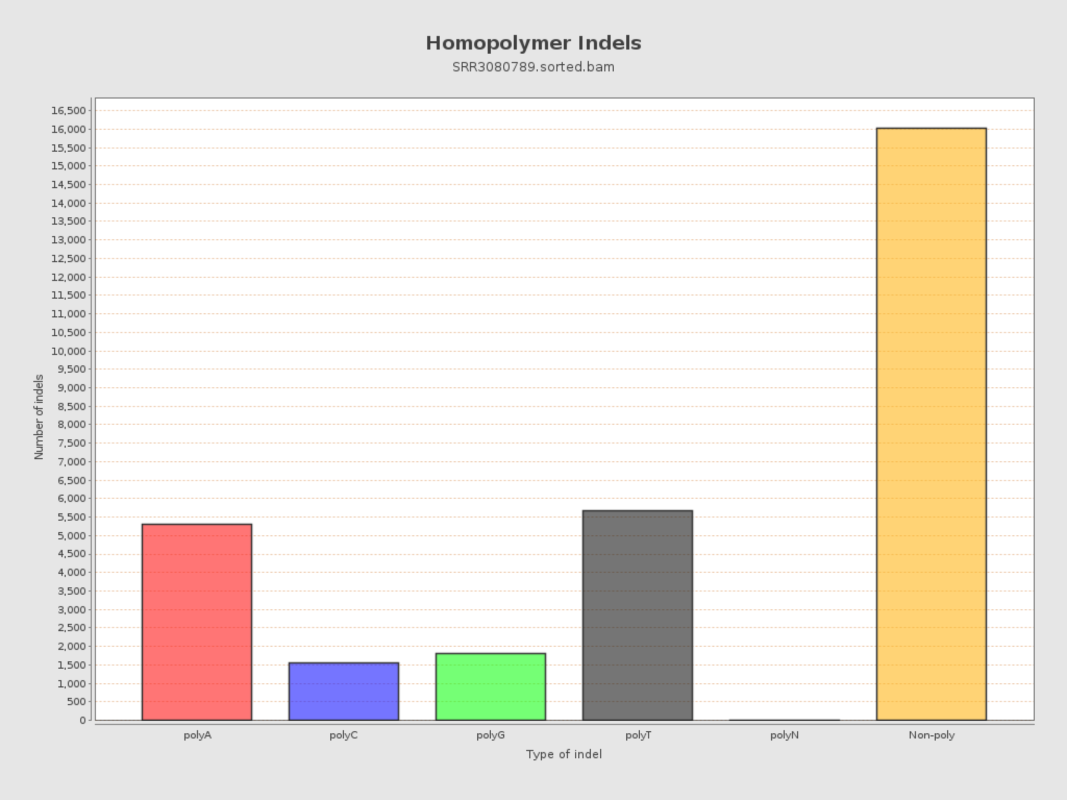
9. Results : Mapped Reads GC-content Distribution



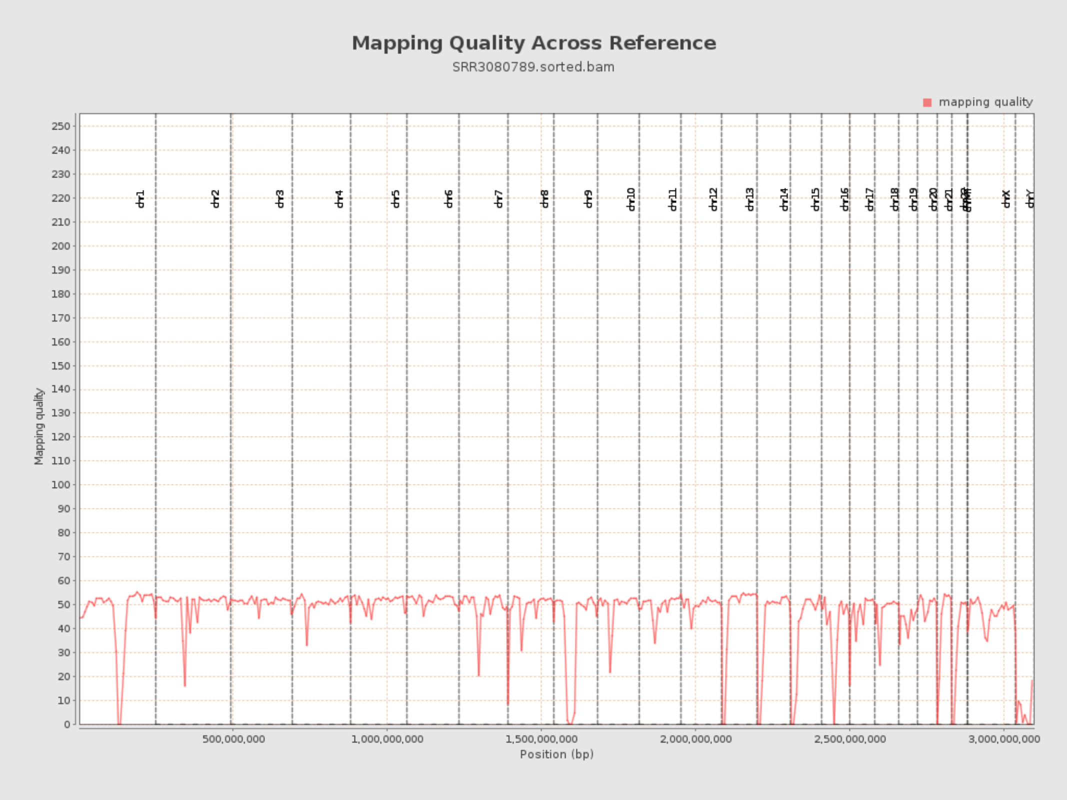
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram